

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/469,637ADATE: 07/16/97  
TIME: 13:11:58

INPUT SET: S19007.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: GREENE, JOHN M  
FLEISCHMANN, ROBERT D

(ii) TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR

(iii) NUMBER OF SEQUENCES: 10

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
(B) STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
(C) CITY: WASHINGTON  
(D) STATE: DC  
(E) COUNTRY: US  
(F) ZIP: 20005-3934

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/469,637  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: STEFFE, ERIC K  
(B) REGISTRATION NUMBER: 36,688  
(C) REFERENCE/DOCKET NUMBER: 1488.0710001

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 371-2600  
(B) TELEFAX: (202) 371 2540

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1527 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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47 (D) TOPOLOGY: linear  
48  
49 (ii) MOLECULE TYPE: DNA (genomic)  
50  
51  
52 (ix) FEATURE:  
53 (A) NAME/KEY: CDS  
54 (B) LOCATION: 46..1248  
55  
56 (ix) FEATURE:  
57 (A) NAME/KEY: sig\_peptide  
58 (B) LOCATION: 46..106  
59  
60 (ix) FEATURE:  
61 (A) NAME/KEY: mat\_peptide  
62 (B) LOCATION: 109..1248  
63  
64  
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
66  
67 CGCCCAGCCG CCGCCTCCAA GCCCCTGAGG TTTCCGGGGA CCACA ATG AAC AAG 54  
68 Met Asn Lys  
69 -21 -20  
70  
71 TTG CTG TGC TGC GCG CTC GTG TTT CTG GAC ATC TCC ATT AAG TGG ACC 102  
72 Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr  
73 -15 -10 -5  
74  
75 ACC CAG GAA ACG TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC 150  
76 Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr  
77 1 5 10  
78  
79 TCT CAT CAG CTG TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA 198  
80 Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys  
81 15 20 25 30  
82  
83 CAA CAC TGT ACA GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC 246  
84 Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp  
85 35 40 45  
86  
87 CAC TAC TAC ACA GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC 294  
88 His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys  
89 50 55 60  
90  
91 AGC CCC GTG TGC AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC 342  
92 Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg  
93 65 70 75  
94  
95 ACC CAC AAC CGC GTG TGC AAA TGC AAG GAA GGG CGC TAC CTT GAG ATA 390  
96 Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile  
97 80 85 90  
98  
99 GAG TTC TGC TTG AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG 438

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100	Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val	
101	95 100 105 110	
102		
103	CAA GCT GGA ACC CCA GAG CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT	486
104	Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp	
105	115 120 125	
106		
107	GGG TTC TTC TCA AAT GAG ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC	534
108	Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His	
109	130 135 140	
110		
111	ACA AAT TGC AGT GTC TTT GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA	582
112	Thr Asn Cys Ser Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala	
113	145 150 155	
114		
115	ACA CAC GAC AAC ATA TGT TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT	630
116	Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys	
117	160 165 170	
118		
119	GGA ATA GAT GTT ACC CTG TGT GAG GAG GCA TTC TTC AGG TTT GCT GTT	678
120	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val	
121	175 180 185 190	
122		
123	CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT GTC TTG GTA GAC AAT TTG	726
124	Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu	
125	195 200 205	
126		
127	CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA GAG AGG ATA AAA CGG CAA	774
128	Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln	
129	210 215 220	
130		
131	CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG CTG AAG TTA TGG AAA CAT	822
132	His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His	
133	225 230 235	
134		
135	CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG ATC ATC CAA GAT ATT GAC	870
136	Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp	
137	240 245 250	
138		
139	CTC TGT GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT AAC CTC ACC	918
140	Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr	
141	255 260 265 270	
142		
143	TTC GAG CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA AAG AAA GTG	966
144	Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val	
145	275 280 285	
146		
147	GGA GCA GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA CCC AGT GAC	1014
148	Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp	
149	290 295 300	
150		
151	CAG ATC CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT GGC GAC CAA	1062
152	Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln	

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153          305          310          315
154
155 GAC ACC TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA AAG ACG TAC      1110
156 Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr
157          320          325          330
158
159 CAC TTT CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC ATC AGG TTC      1158
160 His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe
161 335          340          345          350
162
163 CTT CAC AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA TTT TTA GAA      1206
164 Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu
165          355          360          365
166
167 ATG ATA GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA      1248
168 Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
169          370          375          380
170
171 TAACTGGAAA TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGAGTAA      1308
172
173 ACTGTTTCTC AGGCACTTGA GGCTTTCAGT GATATCTTTC TCATTACCAG TGACTAATTT      1368
174
175 TGCCACAGGG TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT CCTCCAATAA      1428
176
177 ACCCCAAATG GTTAATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT ATATTTTCCC      1488
178
179 TTATTACTGC TTGCAGTAAT TCAACTGGAA AAAAAAAAAA      1527
180
181
182 (2) INFORMATION FOR SEQ ID NO:2:
183
184 (i) SEQUENCE CHARACTERISTICS:
185 (A) LENGTH: 401 amino acids
186 (B) TYPE: amino acid
187 (D) TOPOLOGY: linear
188
189 (ii) MOLECULE TYPE: protein
190
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
192
193 Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
194 -21 -20          -15          -10
195
196 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
197 -5          1          5          10
198
199 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
200          15          20          25
201
202 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
203          30          35          40
204
205 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys

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206	45	50	55
207			
208	Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu		
209	60	65	70 75
210			
211	Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr		
212		80	85 90
213			
214	Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe		
215		95	100 105
216			
217	Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg		
218		110	115 120
219			
220	Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys		
221		125	130 135
222			
223	Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys		
224		140	145 150 155
225			
226	Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr		
227		160	165 170
228			
229	Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg		
230		175	180 185
231			
232	Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val		
233		190	195 200
234			
235	Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
236		205	210 215
237			
238	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu		
239		220	225 230 235
240			
241	Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln		
242		240	245 250
243			
244	Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala		
245		255	260 265
246			
247	Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly		
248		270	275 280
249			
250	Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys		
251		285	290 295
252			
253	Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn		
254		300	305 310 315
255			
256	Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser		
257		320	325 330
258			

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/469,637A**

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Original Text